

# SEQUENCE LISTING

<110> Chiaur, D.  
Pagano, M.  
Latres, E.

<120> NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS

<130> 5914-081

<140> 09/385,219

<141> 1999-08-27

<150> 60/098,355

<151> 1998-08-28

<150> 60/118,568

<151> 1999-02-03

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<151> 1999-03-15

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<170> PatentIn Ver. 2.0

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100

105

110

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 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg  
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 420 425 430  
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 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp  
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 Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu  
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 Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr Cys  
 65 70 75 80  
 Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile Ser Ala Cys Thr Glu  
 85 90 95  
 Val Trp Gln Thr Ala Cys Lys Asn Leu Gly Trp Gln Ile Asp Asp Ser  
 100 105 110  
 Val Gln Asp Ala Leu His Trp Lys Lys Val Tyr Leu Lys Ala Ile Leu  
 115 120 125

Arg Met Lys Gln Leu Glu Asp His Glu Ala Phe Glu Thr Ser Ser Leu  
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 180 185 190  
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 Ala Cys Trp Glu Trp Ser Ser Gly Ala Arg Thr Gln His Phe Arg Gly  
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 His Thr Gly Ala Val Phe Ser Val Asp Tyr Asn Asp Glu Leu Asp Ile  
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<212> PRT

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      20             25             30

Thr Cys Asp Trp Gly Asn Leu Leu Gln Asp Ile Ile Leu Gln Val Phe
      35             40             45

Lys Tyr Leu Pro Leu Leu Asp Arg Ala His Ala Ser Gln Val Cys Arg
      50             55             60

Asn Trp Asn Gln Val Phe His Met Pro Asp Leu Trp Arg Cys Phe Glu
      65             70             75             80

Phe Glu Leu Asn Gln Pro Ala Thr Ser Tyr Leu Lys Ala Thr His Pro
      85             90             95

Glu Leu Ile Lys Gln Ile Ile Lys Arg His Ser Asn His Leu Gln Tyr
      100            105            110

Val Ser Phe Lys Val Asp Ser Ser Lys Glu Ser Ala Glu Ala Ala Cys
      115            120            125

Asp Ile Leu Ser Gln Leu Val Asn Cys Ser Leu Lys Thr Leu Gly Leu
      130            135            140
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 Val Ala Asn Asn Ser Asp Thr Leu Lys Leu Leu Lys Met Ser Ser Cys  
 195 200 205  
 Pro His Val Ser Pro Ala Gly Ile Leu Cys Val Ala Asp Gln Cys His  
 210 215 220  
 Gly Leu Arg Glu Leu Ala Leu Asn Tyr His Leu Leu Ser Asp Glu Leu  
 225 230 235 240  
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 Ile Asp Val Val Ser Glu Asn Pro Gly Gln Thr His Phe His Thr Ile  
 260 265 270  
 Gln Lys Ser Ser Trp Asp Ala Phe Ile Arg His Ser Pro Lys Val Asn  
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 Leu Val Met Tyr Phe Phe Leu Tyr Glu Glu Glu Phe Asp Pro Phe Phe  
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 Arg Tyr Glu Ile Pro Ala Thr His Leu Tyr Phe Gly Arg Ser Val Ser  
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 Lys Asp Val Leu Gly Arg Val Gly Met Thr Cys Pro Arg Leu Val Glu  
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 370 375 380  
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<210> 8

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<212> PRT

<213> Homo sapiens

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Thr Phe Trp Gln Ser Val Ser Lys Asp Arg Val Ala Arg Thr Thr Ser
 35          40          45
Arg Glu Glu Val Asp Glu Ala Ala Ser Thr Leu Thr Arg Leu Pro Ile
 50          55          60
Asp Val Gln Leu Tyr Ile Leu Ser Phe Leu Ser Pro His Asp Leu Cys
 65          70          75          80
Gln Leu Gly Ser Thr Asn His Tyr Trp Asn Glu Thr Val Arg Asn Pro
 85          90          95
Ile Leu Trp Arg Tyr Phe Leu Leu Arg Asp Leu Pro Ser Trp Ser Ser
100          105          110
Val Asp Trp Lys Ser Leu Pro Tyr Leu Gln Ile Leu Lys Lys Pro Ile
115          120          125
Ser Glu Val Ser Asp Gly Ala Phe Phe Asp Tyr Met Ala Val Tyr Leu
130          135          140
Met Cys Cys Pro Tyr Thr Arg Arg Ala Ser Lys Ser Ser Arg Pro Met
145          150          155          160

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 195 200 205  
 Leu Pro Gln Arg Gln Ile Asp Gly Ile Gly Ser Gly Val Asn Phe Gln  
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 225 230 235 240  
 Arg Lys Glu Arg Asp Arg Ala Arg Glu Glu His Thr Ser Ala Val Asn  
 245 250 255  
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 260 265 270  
 Tyr Ser Val Ile Pro Gln Ile Gln Lys Leu Cys Glu Val Val Asp Gly  
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 Phe Ile Tyr Val Ala Asn Ala Glu Ala His Lys Arg His Glu Trp Gln  
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 325 330 335  
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 420 425 430  
 Tyr Tyr Phe Tyr Phe Leu Pro Ile Asn Tyr Lys Lys Arg Val Ser Val  
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Leu His Arg Asn Leu Leu Arg Asn Pro Cys Ala Glu Asn Asp Met Phe 130 135 140		
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<213> Homo sapiens

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Leu Ile Cys Leu Ile Leu His Asp Asp Ile Pro Pro Pro Asn Ile Pro
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Ser Ser Thr Asp Ser Glu His Ser Ser Leu Gln Asn Asn Glu Gln Pro
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Ser Leu Ala Thr Ser Ser Asn Gln Thr Ser Ile Gln Asp Glu Gln Pro
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Ser Asp Ser Phe Gln Gly Gln Ala Ala Gln Ser Gly Val Trp Asn Asp
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Asp Ser Met Leu Gly Pro Ser Gln Asn Phe Glu Ala Glu Ser Ile Gln
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Asp Asn Ala His Met Ala Glu Gly Thr Gly Phe Tyr Pro Ser Glu Pro

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Val 165	Leu Ile His Leu Leu Met Leu Glu Ser Gly Tyr Ile Pro Gln Gly 175			
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Val 195	Tyr Lys Leu Gln Tyr Met His His Leu Cys Glu Gly Ser Ser Ala 205			
Thr 210	Leu Thr Cys Val Pro Leu Gly Asn Leu Ile Val Val Asn Ala Thr 220			
Leu 225	Lys Ile Asn Asn Glu Ile Arg Ser Val Lys Arg Leu Gln Leu Leu 240			
Pro 245	Glu Ser Phe Ile Cys Lys Glu Lys Leu Gly Glu Asn Val Ala Asn 255			
Ile 260	Tyr Lys Asp Leu Gln Lys Leu Ser Arg Leu Phe Lys Asp Gln Leu 270			
Val 275	Tyr Pro Leu Leu Ala Phe Thr Arg Gln Ala Leu Asn Leu Pro Asn 285			
Val 290	Phe Gly Leu Val Val Leu Pro Leu Glu Leu Lys Leu Arg Ile Phe 300			
Arg 305	Leu Leu Asp Val Arg Ser Val Leu Ser Leu Ser Ala Val Cys Arg 320			
Asp 325	Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp Arg Phe Leu Tyr 335			
Leu 340	Arg Asp Phe Arg Asp Asn Thr Val Arg Val Gln Asp Thr Asp Trp 350			
Lys 355	Glu Leu Tyr Arg Lys Arg His Ile Gln Arg Lys Glu Ser Pro Lys 365			
Gly 370	Arg Phe Val Leu Leu Leu Pro Ser Ser Thr His Thr Ile Pro Phe 380			
Tyr 385	Pro Asn Pro Leu His Pro Arg Pro Phe Pro Ser Ser Arg Leu Pro 400			
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Val 420	Gly Asp Pro Ile Ser Ser Leu Ile Pro Gly Pro Gly Glu Thr Pro 430			
Ser 435	Gln Leu Pro Pro Leu Arg Pro Arg Phe Asp Pro Val Gly Pro Leu 445			

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His Met Pro Asp Leu Trp Arg  
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<213> Homo sapiens

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Arg Asn Pro Ile Leu Trp Arg  
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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu Asp Arg Ala Cys  
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 Ala Leu Gly Leu Ser Lys Cys Glu Val Ser Cys Ser Ala Phe Ile Arg  
 370 375 380

Phe Val Arg Leu Cys Glu Arg Arg Leu Thr Gln Leu Ser Val Met Glu  
385 390 395 400

Glu Val Leu Ile Pro Asp Glu Asp Tyr Ser Leu Asp Glu Ile His Thr  
405 410 415

Glu Val Ser Lys Tyr Leu Gly Arg Val Trp Phe Pro Asp Val Met Pro  
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Leu Trp

<210> 25

<211> 1970

<212> DNA

<213> Homo sapiens

<400> 25

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<210> 26

<211> 634

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 26

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20 25 30  
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35 40 45  
Leu Gly Thr Ser Ser Arg Leu Ser His Phe Pro Phe Gly Lys Ser Pro  
50 55 60  
Pro Arg Gly Gln Phe Val Ala Ala Ala Val Glu Ile Ala Gly Arg Ser  
65 70 75 80  
Gly Leu Gln Met Gly Gln Gly Leu Trp Arg Val Val Arg Asn Gln Gln  
85 90 95  
Leu Gln Gln Glu Gly Tyr Ser Glu Gln Gly Tyr Leu Thr Arg Glu Gln  
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Ser Arg Arg Met Ala Ala Ser Asn Ile Ser Asn Thr Asn His Arg Lys  
115 120 125  
Gln Val Gln Gly Gly Ile Asp Ile Tyr His Leu Leu Lys Ala Arg Lys  
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Ser Lys Glu Gln Glu Gly Phe Ile Asn Leu Glu Met Leu Pro Pro Glu  
145 150 155 160  
Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr Asp Leu Cys Leu  
165 170 175  
Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu Leu Leu Trp Gln  
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195 200 205  
Pro Pro Leu Gly Phe Ser Phe Arg Lys Xaa Tyr Met Gln Leu Asp Glu  
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Gly Ser Leu Thr Phe Asn Ala Asn Pro Asp Glu Gly Val Asn Tyr Phe  
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Ile Phe Cys Thr Arg Thr Leu Asn Trp Lys Lys Leu Arg Ile Tyr Leu  
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Asp Glu Arg Arg Asp Val Leu Asp Asp Leu Val Thr Leu His Asn Phe  
275 280 285  
Arg Asn Gln Phe Leu Pro Asn Ala Leu Arg Glu Phe Phe Arg His Ile  
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His Ala Pro Glu Glu Arg Gly Glu Tyr Leu Glu Thr Leu Ile Thr Lys

305                      310                      315                      320  
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 Val His Ile Cys Leu Lys Asn Phe Ile His Phe His Ser Leu Tyr Lys  
                                  500                      505                      510  
 Tyr His Val Met Cys Thr Tyr Leu Thr Lys Glu Ile Tyr Ser His Asn  
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 Arg Val Leu Ile Cys Tyr Tyr Ile Thr Met Gln Asn Trp Gln Leu Phe  
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 Leu Tyr Lys Phe Ile Ile Phe Phe Ile Leu Lys Thr Gly Leu Ile Lys  
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 Ser Arg Val Leu Thr Ile Asp Phe Asn Ile Lys Ile Tyr Asp Leu His  
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<210> 27  
<211> 4168

<212> DNA

<213> Homo sapiens

<400> 27

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gttcttttca	gagcacgttc	cttgtaattg	cttcagtgac	attgagaacc	ttgaaggacc	420
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<210> 28

<211> 621

<212> PRT

<213> Homo sapiens

<400> 28

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Leu	Pro	Gly	Glu	Val	Leu	Glu	Tyr	Ile	Leu	Cys	Cys	Gly	Ser	Leu	Thr	35	40	45	
Ala	Ala	Asp	Ile	Gly	Arg	Val	Ser	Ser	Thr	Cys	Arg	Arg	Leu	Arg	Glu	50	55	60	
Leu	Cys	Gln	Ser	Ser	Gly	Lys	Val	Trp	Lys	Glu	Gln	Phe	Arg	Val	Arg	65	70	75	80
Trp	Pro	Ser	Leu	Met	Lys	His	Tyr	Ser	Pro	Thr	Asp	Tyr	Val	Asn	Trp	85	90	95	
Leu	Glu	Glu	Tyr	Lys	Val	Arg	Gln	Lys	Ala	Gly	Leu	Glu	Ala	Arg	Lys	100	105	110	
Ile	Val	Ala	Ser	Phe	Ser	Lys	Arg	Phe	Phe	Ser	Glu	His	Val	Pro	Cys	115	120	125	
Asn	Gly	Phe	Ser	Asp	Ile	Glu	Asn	Leu	Glu	Gly	Pro	Glu	Ile	Phe	Phe	130	135	140	
Glu	Asp	Glu	Leu	Val	Cys	Ile	Leu	Asn	Met	Glu	Gly	Arg	Lys	Ala	Leu	145	150	155	160
Thr	Trp	Lys	Tyr	Tyr	Ala	Lys	Lys	Ile	Leu	Tyr	Tyr	Leu	Arg	Gln	Gln	165	170	175	
Lys	Ile	Leu	Asn	Asn	Leu	Lys	Ala	Phe	Leu	Gln	Gln	Pro	Asp	Asp	Tyr	180	185	190	
Glu	Ser	Tyr	Leu	Glu	Gly	Ala	Val	Tyr	Ile	Asp	Gln	Tyr	Cys	Asn	Pro				





Asn Met Asn Val His Ser Leu Pro His Gly His His Gln Pro Phe Tyr  
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 545 550 555 560  
 Leu Glu Tyr Asn Val Glu Pro Gln Glu Ile Ser His Pro Asp Val Gly  
 565 570 575  
 Arg Tyr Phe Ser Glu Phe Thr Gly Thr His Tyr Ile Pro Asn Ala Glu  
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<210> 29  
 <211> 278  
 <212> DNA  
 <213> Homo sapiens

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 <222> all n positions  
 <223> n=a, c, g or t

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 ggagcgtgtg ctcaccttcc tgcccggccaa ggcgttgctg cgggtggcct gcgtgtgccg 180  
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<210> 30  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> all Xaa positions  
 <223> Xaa=unknown amino acid residue

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 Ser Asn Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala  
 35 40 45  
 Lys Ala Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys  
 50 55 60  
 Val Arg Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile Ser Ala



Asp Pro Asn Leu Trp Lys Arg Leu Tyr Met Glu Val Phe Glu Tyr Thr  
 180 185 190

Arg Pro Met Met His  
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<210> 33  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

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<210> 34  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
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 35 40 45  
 Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu  
 50 55 60  
 Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro  
 65 70 75 80  
 Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu  
 85 90 95  
 Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile  
 100 105 110  
 Cys Phe Ser Leu Phe Arg Arg Arg Arg Glu Arg Arg Thr Leu Ser Val  
 115 120 125  
 Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala  
 130 135 140  
 Ser Leu Tyr Asp Arg Ile Val Leu Phe Pro Gly Val Tyr Glu Glu Gln  
 145 150 155 160  
 Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys

165

170

175

Leu Gly

&lt;210&gt; 35

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

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ggtttgagtc agtacatagc agtggaagct gcagagggtt gaaacaaaaa tgaagttttc 660
taccaatgtc agacagtaga acgtgtgttt aaatatggca ttaagatgtg ttctgatggt 720
tgtataaatg gcatgcatta ggtattttca g 751

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&lt;210&gt; 36

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

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Glu Thr Glu Thr Ala Pro Leu Thr Leu Glu Ser Leu Pro Thr Asp Pro
 1                      5                      10                      15

Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg Asp Leu Ile Asn Cys
      20                      25                      30

Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser Ser His Asp Pro Leu
      35                      40                      45

Trp Arg Arg His Cys Lys Lys Tyr Trp Leu Ile Ser Glu Glu Glu Lys
      50                      55                      60

Thr Gln Lys Asn Gln Cys Trp Lys Ser Leu Phe Ile Asp Thr Tyr Ser
      65                      70                      75                      80

Asp Val Gly Arg Tyr Ile Asp His Tyr Ala Ala Ile Lys Lys Ala Ser
      85                      90                      95

Gly Met Ile Ser Arg Asn Ile Trp Ser Pro Gly Val Leu Gly Trp Val
      100                      105                      110

Leu Ser Leu Lys Glu Gly Cys Ser Arg Gly Arg Pro Arg Cys Cys Gly
      115                      120                      125

Ser Ala Asp Trp Ala Ala Ser Phe Leu Asp Asp Tyr Arg Cys Ser Tyr
      130                      135                      140

Arg Ile His Asn Gly Gln Lys Leu Val Gly Ser Trp Gly Tyr Trp Glu
      145                      150                      155                      160

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Ala Trp His Cys Leu Ile Thr Ile Val Leu Lys Ile Cys Thr Ser Ile  
 165 170 175  
 Gln Leu Pro Glu Ile Pro Ala Glu Thr Gly Thr Glu Ile Leu Ser Pro  
 180 185 190  
 Phe Asn Phe Cys Ile His Thr Gly Leu Ser Gln Tyr Ile Ala Val Glu  
 195 200 205  
 Ala Ala Glu Gly Asn Lys Asn Glu Val Phe Tyr Gln Cys Gln Thr Val  
 210 215 220  
 Glu Arg Val Phe Lys Tyr Gly Ile Lys Met Cys Ser Asp Gly Cys Ile  
 225 230 235 240  
 Asn Gly Met His Val Phe Ser  
 245

<210> 37  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> all n positions  
 <223> n=a, c, g or t

<400> 37  
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 caggaacctg aggtcggctg ctgcgggaaa tacttcctgt ttggcttcaa cattgtcttc 120  
 tgggtgctgg gagccctgtt cctggctatc ggccctctggg cctgggggtga gaagggcggt 180  
 ctctcgaaca tctcagcgt gacagatctg ggaggccttg accccgtgtg gcttggtttgt 240  
 ggtagttgga ggcgtcatgt cgggtgctggg ctttgctggg ctgcaattgg ggccctccgg 300  
 gagaacacct tctgctcaa gtttttctnc gngttcctcg gtctcatctt ctctctggag 360  
 ctggcaac 368

<210> 38  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> all Xaa positions  
 <223> Xaa=unknown amino acid residue

<400> 38  
 Gly Ser Gly Phe Arg Ala Gly Gly Trp Pro Leu Thr Met Pro Gly Lys  
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 His Gln His Phe Gln Glu Pro Glu Val Gly Cys Cys Gly Lys Tyr Phe  
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 Leu Phe Gly Phe Asn Ile Val Phe Trp Val Leu Gly Ala Leu Phe Leu  
 35 40 45  
 Ala Ile Gly Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile  
 50 55 60

Ser Ala Leu Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys  
65 70 75 80

Gly Ser Trp Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala Ala Ile  
85 90 95

Gly Ala Leu Arg Glu Asn Thr Phe Leu Leu Lys Phe Phe Xaa Xaa Phe  
100 105 110

Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala  
115 120

<210> 39  
<211> 774  
<212> DNA  
<213> Homo sapiens

<400> 39  
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accacgatg agagcgtcaa gaagtacttc gcctcctcct ttgagtgggtg tcgcaaagca 420  
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gccatcgttg tgaaggactg gtactcgggc cgcagcgacg ctggttgcct ctacgagctc 540  
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gcagtgcccc aagacagtga cggcgggggc tggatggaga tctccacac cttcaccgac 660  
tacgggcccg gcgtccgctt cgtccgcttc gagcacgggg ggcagggctc cgtctactgg 720  
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<210> 40  
<211> 257  
<212> PRT  
<213> Homo sapiens

<400> 40  
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1 5 10 15

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20 25 30

Arg Leu Val Cys Leu Arg Trp Lys Glu Leu Val Asp Gly Ala Pro Leu  
35 40 45

Trp Leu Leu Lys Cys Gln Gln Glu Gly Leu Val Pro Glu Gly Gly Val  
50 55 60

Glu Glu Glu Arg Asp His Trp Gln Gln Phe Tyr Phe Leu Ser Lys Arg  
65 70 75 80

Arg Arg Asn Leu Leu Arg Asn Pro Cys Gly Glu Glu Asp Leu Glu Gly  
85 90 95

Trp Cys Asp Val Glu His Gly Gly Asp Gly Trp Arg Val Glu Leu  
100 105 110

Pro Gly Asp Ser Gly Val Glu Phe Thr His Asp Glu Ser Val Lys Lys  
115 120 125

Tyr Phe Ala Ser Ser Phe Glu Trp Cys Arg Lys Ala Gln Val Ile Asp  
130 135 140

Leu Gln Ala Glu Gly Tyr Trp Glu Glu Leu Leu Asp Thr Thr Gln Pro  
145 150 155 160

Ala Ile Val Val Lys Asp Trp Tyr Ser Gly Arg Ser Asp Ala Gly Cys  
165 170 175

Leu Tyr Glu Leu Thr Val Lys Leu Leu Ser Glu His Glu Asn Val Leu  
180 185 190

Ala Glu Phe Ser Ser Gly Gln Val Ala Val Pro Gln Asp Ser Asp Gly  
195 200 205

Gly Gly Trp Met Glu Ile Ser His Thr Phe Thr Asp Tyr Gly Pro Gly  
210 215 220

Val Arg Phe Val Arg Phe Glu His Gly Gly Gln Gly Ser Val Tyr Trp  
225 230 235 240

Lys Gly Trp Phe Gly Ala Arg Val Thr Asn Ser Ser Val Trp Val Glu  
245 250 255

Pro

<210> 41

<211> 957

<212> DNA

<213> Homo sapiens

<400> 41

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ttgttcccc cagagctggt ggagcatatc atctcattcc tcccagtcag agaccttggt 180
gccctcggcc agacctgccc ctacttccac gaagtgtgcg atggggaagg cgtgtggaga 240
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gtcttcaaga tgacattcca ccactcaatg accttcaagc agatcgtgct ggttggtcag 720
gagaccagc gggctctact gctcctcaca gaggaaggaa agatctactc tttggtagtg 780
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tcccactacc tgcctcacct gcgcgtggcc tgcagtactt ccaaccagag cagcaccctc 900
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<210> 42

<211> 318

<212> PRT

<213> Homo sapiens

<400> 42

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Lys Gly Asn Pro Ile Ser Ile Gln Leu Phe Pro Pro Glu Leu Val Glu	35	40	45
His Ile Ile Ser Phe Leu Pro Val Arg Asp Leu Val Ala Leu Gly Gln	50	55	60
Thr Cys Arg Tyr Phe His Glu Val Cys Asp Gly Glu Gly Val Trp Arg	65	70	75
Arg Ile Cys Arg Arg Leu Ser Pro Arg Leu Gln Asp Gln Asp Thr Lys	85	90	95
Gly Leu Tyr Phe Gln Ala Phe Gly Gly Arg Arg Arg Cys Leu Ser Lys	100	105	110
Ser Val Ala Pro Leu Leu Ala His Gly Tyr Arg Arg Phe Leu Pro Thr	115	120	125
Lys Asp His Val Phe Ile Leu Asp Tyr Val Gly Thr Leu Phe Phe Leu	130	135	140
Lys Asn Ala Leu Val Ser Thr Leu Gly Gln Met Gln Trp Lys Arg Ala	145	150	155
Cys Arg Tyr Val Val Leu Cys Arg Gly Ala Lys Asp Phe Ala Ser Asp	165	170	175
Pro Arg Cys Asp Thr Val Tyr Arg Lys Tyr Leu Tyr Val Leu Ala Thr	180	185	190
Arg Glu Pro Gln Glu Val Val Gly Thr Thr Ser Ser Arg Ala Cys Asp	195	200	205
Cys Val Glu Val Tyr Leu Gln Ser Ser Gly Gln Arg Val Phe Lys Met	210	215	220
Thr Phe His His Ser Met Thr Phe Lys Gln Ile Val Leu Val Gly Gln	225	230	235
Glu Thr Gln Arg Ala Leu Leu Leu Leu Thr Glu Glu Gly Lys Ile Tyr	245	250	255
Ser Leu Val Val Asn Glu Thr Gln Leu Asp Gln Pro Arg Ser Tyr Thr	260	265	270
Val Gln Leu Ala Leu Arg Lys Val Ser His Tyr Leu Pro His Leu Arg	275	280	285
Val Ala Cys Met Thr Ser Asn Gln Ser Ser Thr Leu Tyr Val Thr Asp	290	295	300
Pro Ile Leu Cys Ser Trp Leu Gln Pro Pro Trp Pro Gly Gly	305	310	315

<210> 43

<211> 1590  
 <212> DNA  
 <213> Homo sapiens

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 ggggctgagg cgggagcgag gacacgcca agagaggaag cagagggagg cggaaagcgtg 180  
 gaggaagggg cgagagggcat catcaaagga gatgagggga gcgtaggggc cgggaaagag 240  
 gcacaaggaa gaaagtatgg gaaggaggaa tggaggggtca gggctaggcg gcgggagggc 300  
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 cacttcacca actgcgacct gctccggcgc cagatagcct gggcctcgct caactccggc 600  
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 agccctgtgt actgcctgca tctcaccacc aagcatctct atgctgcgct gtcttacaac 1560  
 ctccacgtcc tggatattca aaaccctgta 1590

<210> 44  
 <211> 529  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Arg Gly Gly Ser Glu Gly Arg Gly Arg Gly Arg Glu Lys Arg Ala Arg  
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 20 25 30  
 Asp Gly Glu Gly Gly Ser Gly Pro Gly Ala Glu Ala Gly Ala Arg Thr  
 35 40 45  
 Arg Pro Arg Glu Glu Ala Glu Gly Gly Gly Ser Val Glu Glu Gly Ala  
 50 55 60  
 Arg Gly Ile Ile Lys Gly Asp Glu Gly Ser Val Gly Ala Gly Lys Glu  
 65 70 75 80  
 Ala Gln Gly Arg Lys Tyr Gly Lys Glu Glu Trp Arg Val Arg Ala Arg  
 85 90 95  
 Arg Arg Glu Gly Ala Arg Pro Gly Arg Val Gln Gly Gln Gly Gly Gln  
 100 105 110  
 Val Trp Ala Tyr Ile Pro Gly Thr Gly Ala Ala Met Ala Ala Ala Ala

115						120						125					
Arg	Glu	Glu	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Ser	Ala	Ala	Cys	Pro	Ala		
130						135					140						
Ala	Gly	Pro	Ala	Leu	Trp	Arg	Leu	Pro	Glu	Val	Leu	Leu	Leu	His	Met		
145					150					155					160		
Cys	Ser	Tyr	Leu	Asp	Met	Arg	Ala	Leu	Gly	Arg	Leu	Ala	Gln	Val	Tyr		
				165					170					175			
Arg	Trp	Leu	Trp	His	Phe	Thr	Asn	Cys	Asp	Leu	Leu	Arg	Arg	Gln	Ile		
			180					185						190			
Ala	Trp	Ala	Ser	Leu	Asn	Ser	Gly	Phe	Thr	Arg	Leu	Gly	Thr	Asn	Leu		
		195					200					205					
Met	Thr	Ser	Val	Pro	Val	Lys	Val	Ser	Gln	Asn	Trp	Ile	Val	Gly	Cys		
						215					220						
Cys	Arg	Glu	Gly	Ile	Leu	Leu	Lys	Trp	Arg	Cys	Ser	Gln	Met	Pro	Trp		
225					230					235					240		
Met	Gln	Leu	Glu	Asp	Asp	Ala	Leu	Tyr	Ile	Ser	Gln	Ala	Asn	Phe	Ile		
				245					250					255			
Leu	Ala	Tyr	Gln	Phe	Arg	Pro	Asp	Gly	Ala	Ser	Leu	Asn	Arg	Gln	Pro		
			260					265						270			
Leu	Gly	Val	Ser	Ala	Gly	His	Asp	Glu	Asp	Val	Cys	His	Phe	Val	Leu		
		275					280					285					
Ala	Thr	Ser	His	Ile	Val	Ser	Ala	Gly	Gly	Asp	Gly	Lys	Ile	Gly	Leu		
						295					300						
Gly	Lys	Ile	His	Ser	Thr	Phe	Ala	Ala	Lys	Tyr	Trp	Ala	His	Glu	Gln		
305					310					315					320		
Glu	Val	Asn	Cys	Val	Asp	Cys	Lys	Gly	Gly	Ile	Ile	Ser	Phe	Gly	Ser		
				325					330					335			
Arg	Asp	Arg	Thr	Ala	Lys	Val	Trp	Pro	Leu	Ala	Ser	Gly	Gln	Leu	Gly		
			340					345						350			
Gln	Cys	Leu	Tyr	Thr	Ile	Gln	Thr	Glu	Asp	Gln	Ile	Trp	Ser	Val	Ala		
		355					360					365					
Ile	Arg	Pro	Leu	Leu	Ser	Ser	Phe	Val	Thr	Gly	Thr	Ala	Cys	Cys	Gly		
		370					375					380					
His	Phe	Ser	Pro	Leu	Lys	Ile	Trp	Asp	Leu	Asn	Ser	Gly	Gln	Leu	Met		
385					390					395					400		
Thr	His	Leu	Asp	Arg	Asp	Phe	Pro	Pro	Arg	Ala	Gly	Val	Leu	Asp	Val		
				405					410					415			
Ile	Tyr	Glu	Ser	Pro	Phe	Ala	Leu	Leu	Ser	Cys	Gly	Tyr	Asp	Thr	Tyr		
			420				425						430				
Val	Arg	Tyr	Trp	Asp	Cys	Arg	Thr	Ser	Val	Arg	Lys	Cys	Val	Met	Glu		
			435				440					445					

Trp Glu Glu Pro His Asn Ser Thr Leu Tyr Cys Leu Gln Thr Asp Gly  
450 455 460

Asn His Leu Leu Ala Thr Gly Ser Ser Phe Tyr Ser Val Val Arg Leu  
465 470 475 480

Trp Asp Arg His Gln Arg Ala Cys Pro His Thr Phe Pro Leu Thr Ser  
485 490 495

Thr Arg Leu Gly Ser Pro Val Tyr Cys Leu His Leu Thr Thr Lys His  
500 505 510

Leu Tyr Ala Ala Leu Ser Tyr Asn Leu His Val Leu Asp Ile Gln Asn  
515 520 525

Pro

<210> 45  
<211> 1214  
<212> DNA  
<213> Homo sapiens

<400> 45  
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gcaccttggg agaagccttt aatcgggttag acttctcaag tgcaattcaa gatatccgaa 240  
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ttgcgtactc tctc 1214

<210> 46  
<211> 272  
<212> PRT  
<213> Homo sapiens

<400> 46  
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Leu Gly Glu Ala Phe Asn Arg Leu Asp Phe Ser Ser Ala Ile Gln Asp  
20 25 30

Ile Arg Thr Phe Asn Tyr Val Val Lys Leu Leu Gln Leu Ile Ala Lys



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<210> 48  
 <211> 483  
 <212> PRT  
 <213> Homo sapiens

<400> 48

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Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro	35	40	45	
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly	50	55	60	
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val	65	70	75	80
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala	85	90	95	
Ser	Arg	Pro	Gln	Lys	Glu	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His	100	105	110	
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg	115	120	125	
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg	130	135	140	
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg	145	150	155	160
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val	165	170	175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr	180	185	190	
Asp	Arg	Gly	Leu	Tyr	Thr	Ile	Ala	Gln	Cys	Cys	Pro	Glu	Leu	Arg	Arg	195	200	205	
Leu	Glu	Val	Ser	Gly	Cys	Tyr	Asn	Ile	Ser	Asn	Glu	Ala	Val	Phe	Asp	210	215	220	
Val	Val	Ser	Leu	Cys	Pro	Asn	Leu	Glu	His	Leu	Asp	Val	Ser	Gly	Cys	225	230	235	240
Ser	Lys	Val	Thr	Cys	Ile	Ser	Leu	Thr	Arg	Glu	Ala	Ser	Ile	Lys	Leu	245	250	255	
Ser	Pro	Leu	His	Gly	Lys	Gln	Ile	Ser	Ile	Arg	Tyr	Leu	Asp	Met	Thr	260	265	270	
Asp	Cys	Phe	Val	Leu	Glu	Asp	Glu	Gly	Leu	His	Thr	Ile	Ala	Ala	His	275	280	285	
Cys	Thr	Gln	Leu	Thr	His	Leu	Tyr	Leu	Arg	Arg	Cys	Val	Arg	Leu	Thr				

290 295 300  
 Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu  
 305 310 315 320  
 Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu  
 325 330 335  
 Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys  
 340 345 350  
 Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser  
 355 360 365  
 Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His  
 370 375 380  
 Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp  
 385 390 395 400  
 Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala  
 405 410 415  
 Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser  
 420 425 430  
 Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu  
 435 440 445  
 Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg  
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 Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro  
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 Ala Phe Phe

<210> 49  
 <211> 850  
 <212> DNA  
 <213> Homo sapiens

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 gctccaggtg ctgcggctgt tgaacctgat gtggctgccc aagcctccgg gacgaggggt 780  
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 ctttgtgagc 850



<210> 50  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens  
 <400> 50  
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 Gln Ile Phe Gly Leu Leu Val Ala Ala Asp Gly Pro Met Pro Phe Leu  
 35 40 45  
 Gly Arg Ala Ala Arg Val Cys Arg Arg Trp Gln Glu Ala Ala Ser Gln  
 50 55 60  
 Pro Ala Leu Trp His Thr Val Thr Leu Ser Ser Pro Leu Val Gly Arg  
 65 70 75 80  
 Pro Ala Lys Gly Gly Val Lys Ala Glu Lys Lys Leu Leu Ala Ser Leu  
 85 90 95  
 Glu Trp Leu Met Pro Asn Arg Phe Ser Gln Leu Gln Arg Leu Thr Leu  
 100 105 110  
 Ile His Trp Lys Ser Gln Val His Pro Val Leu Lys Leu Val Gly Glu  
 115 120 125  
 Cys Cys Pro Arg Leu Thr Phe Leu Lys Leu Ser Gly Cys His Gly Val  
 130 135 140  
 Thr Ala Asp Ala Leu Val Met Leu Ala Lys Ala Cys Cys Gln Leu His  
 145 150 155 160  
 Ser Leu Asp Leu Gln His Ser Met Val Glu Ser Thr Ala Val Val Ser  
 165 170 175  
 Phe Leu Glu Glu Ala Gly Ser Arg Met Arg Lys Leu Trp Leu Thr Tyr  
 180 185 190  
 Ser Ser Gln Thr Thr Ala Ile Leu Gly Ala Leu Leu Gly Ser Cys Cys  
 195 200 205  
 Pro Gln Leu Gln Val Leu Glu Val Ser Thr Gly Ile Asn Arg Asn Ser  
 210 215 220  
 Ile Pro Leu Gln Leu Pro Val Glu Ala Leu Gln Lys Gly Cys Pro Gln  
 225 230 235 240  
 Leu Gln Val Leu Arg Leu Leu Asn Leu Met Trp Leu Pro Lys Pro Pro  
 245 250 255  
 Gly Arg Gly Val Ala Pro Gly Pro Gly Phe Pro Ser Leu Glu Glu Leu  
 260 265 270  
 Cys Leu Ala Ser Ser Thr Cys Asn Phe Val Ser  
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<210> 51

<211> 1777

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> all n positions

<223> n=a, c, g or t

<400> 51

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agaagtgtca gaacactcca caggataaac ccactcttcc cctgaggtaa tgctgtcaat 180
tttcagctat cttaatcctc aagagttatg tcgatgcagt caagtaagca tgaaatgggtc 240
tcagctgaca aaaacgggat cgctttggaa acatctttac cctgttcatt gggccagagg 300
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atctgaagag tctgcgaggg aatcaattgc tatcagcatt gcacaaatgg aaaaacgttt 480
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taacctggag catctggatc ttaccagac tgacatttca gattctgcat ttgacagttg 660
gtcttggtct gggtgctgcc agagtcttcg gcatcttgat ctgtctggtt gtgagaaaat 720
cacagatgtg gccctagaga agatttccag agctcttgga attctgacat ctcacaaaag 780
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<210> 52

<211> 590

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 52

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          20                      25                      30

Asp Glu Lys Ser Asp Lys Glu Ala Glu Val Ser Glu His Ser Thr Gly
    35                      40                      45
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Ile	Thr	His	Leu	Pro	Pro	Glu	Val	Met	Leu	Ser	Ile	Phe	Ser	Tyr	Leu	50	55	60
Asn	Pro	Gln	Glu	Leu	Cys	Arg	Cys	Ser	Gln	Val	Ser	Met	Lys	Trp	Ser	65	70	75
Gln	Leu	Thr	Lys	Thr	Gly	Ser	Leu	Trp	Lys	His	Leu	Tyr	Pro	Val	His	85	90	95
Trp	Ala	Arg	Gly	Asp	Trp	Tyr	Ser	Gly	Pro	Ala	Thr	Glu	Leu	Asp	Thr	100	105	110
Glu	Pro	Asp	Asp	Glu	Trp	Val	Lys	Asn	Arg	Lys	Asp	Glu	Ser	Arg	Ala	115	120	125
Phe	His	Glu	Trp	Asp	Glu	Asp	Ala	Asp	Ile	Asp	Glu	Ser	Glu	Glu	Ser	130	135	140
Ala	Glu	Glu	Ser	Ile	Ala	Ile	Ser	Ile	Ala	Gln	Met	Glu	Lys	Arg	Leu	145	150	155
Leu	His	Gly	Leu	Ile	His	Asn	Val	Leu	Pro	Tyr	Val	Gly	Thr	Ser	Val	165	170	175
Lys	Thr	Leu	Val	Leu	Ala	Tyr	Ser	Ser	Ala	Val	Ser	Ser	Lys	Met	Val	180	185	190
Arg	Gln	Ile	Leu	Glu	Leu	Cys	Pro	Asn	Leu	Glu	His	Leu	Asp	Leu	Thr			
Gln	Thr	Asp	Ile	Ser	Asp	Ser	Ala	Phe	Asp	Ser	Trp	Ser	Trp	Leu	Gly	210	215	220
Cys	Cys	Gln	Ser	Leu	Arg	His	Leu	Asp	Leu	Ser	Gly	Cys	Glu	Lys	Ile	225	230	235
Thr	Asp	Val	Ala	Leu	Glu	Lys	Ile	Ser	Arg	Ala	Leu	Gly	Ile	Leu	Thr	245	250	255
Ser	His	Gln	Ser	Gly	Phe	Leu	Lys	Thr	Ser	Thr	Ser	Lys	Ile	Thr	Ser	260	265	270
Thr	Ala	Trp	Lys	Asn	Lys	Asp	Ile	Thr	Met	Gln	Ser	Thr	Lys	Gln	Tyr	275	280	285
Ala	Cys	Leu	His	Asp	Leu	Thr	Asn	Lys	Gly	Ile	Gly	Glu	Glu	Ile	Asp	290	295	300
Asn	Glu	His	Pro	Trp	Thr	Lys	Pro	Val	Ser	Ser	Glu	Asn	Phe	Thr	Ser	305	310	315
Pro	Tyr	Val	Trp	Met	Leu	Asp	Ala	Glu	Asp	Leu	Ala	Asp	Ile	Glu	Asp	325	330	335
Thr	Val	Glu	Trp	Arg	His	Arg	Asn	Val	Glu	Ser	Leu	Cys	Val	Met	Glu	340	345	350
Thr	Ala	Ser	Asn	Phe	Ser	Cys	Ser	Thr	Ser	Gly	Cys	Phe	Ser	Lys	Asp	355	360	365
Ile	Val	Gly	Leu	Arg	Thr	Ser	Val	Cys	Trp	Gln	Gln	His	Cys	Ala	Ser	370	375	380

Pro Ala Phe Ala Tyr Cys Gly His Ser Phe Cys Cys Thr Gly Thr Ala  
385 390 395 400

Leu Arg Thr Met Ser Ser Leu Pro Glu Ser Ser Ala Met Cys Arg Lys  
405 410 415

Ala Ala Arg Thr Arg Leu Pro Arg Gly Lys Asp Leu Ile Tyr Phe Gly  
420 425 430

Ser Glu Lys Ser Asp Gln Glu Thr Gly Arg Val Leu Leu Phe Leu Ser  
435 440 445

Leu Ser Gly Cys Tyr Gln Ile Thr Asp His Gly Leu Arg Val Leu Thr  
450 455 460

Leu Gly Gly Gly Leu Pro Tyr Leu Glu His Leu Asn Leu Ser Gly Cys  
465 470 475 480

Leu Thr Ile Thr Gly Ala Gly Leu Gln Asp Leu Val Ser Ala Cys Pro  
485 490 495

Ser Leu Asn Asp Glu Tyr Phe Tyr Tyr Cys Asp Asn Ile Asn Gly Pro  
500 505 510

His Ala Asp Thr Ala Ser Gly Cys Gln Asn Leu Gln Cys Gly Phe Arg  
515 520 525

Ala Cys Cys Arg Ser Gly Glu Pro Leu Thr Ser Asp Leu Cys Leu Leu  
530 535 540

His Leu Ala Glu Gln Ala Phe Phe His Ala Leu Tyr Ser His Ile Ser  
545 550 555 560

Cys Val Asn His Pro Phe Leu Ser Val Thr Cys Phe Gly Pro Ile Xaa  
565 570 575

Tyr Asn Phe Arg Asn Leu Asn Tyr Gln Xaa Ile Val Met Leu  
580 585 590

<210> 53  
<211> 1681  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> all n positions  
<223> n=a, c, g or t

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gagggcaaaa ggagcactag ctaggtcaga gccatgtttc aggtcacaaat gtgatgtcag 180  
atgttgctta taaatccttt cttgtcttcg ccattcttaa atcttgatag gtgcctgttg 240  
ggaaactgta aatgcctttc ccaatggaga atcaacagat tgggtgatgg tggagtcggg 300  
caggaagact caggtcttct agaggaaagg atgcctcatc accccttngg cccaggcagc 360  
tgctgtcaga gaatgacaca gcacctgcac agtcgctgtc cacttcctgc cactgctgtc 420  
gggtggggtga cgggagcaaa gtaggcgtgg actttgacat gagggagctg agcccgcatc 480  
cgcttgatgc ctgcacgggt aacctgctgg cagtcgtaca gctcgaggcg ctccaggcct 540  
cggcagttct ctaggtgtyc cagggccaca tcagtgatga ggaggcagtt gtccaactcc 600

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aagggaaaata ttcttaacag aagttctttg ggtaactttt tgtaataaag gccttcatca 1620
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<210> 54
<211> 437
<212> PRT
<213> Homo sapiens

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<220>
<221> SITE
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<223> Xaa=unknown amino acid residue

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Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg
      35             40             45

Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser
      50             55             60

Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Ile Asp Val Glu Gly
      65             70             75             80

Arg Val Val Glu Asn Ile Ser Lys Arg Cys Val Gly Phe Leu Arg Lys
      85             90             95

Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Asp Ser Ser Leu Lys Thr
      100            105            110

Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys
      115            120            125

Thr Lys Ile Thr Asp Ser Thr Cys Tyr Ser Leu Ser Arg Phe Cys Ser
      130            135            140

Lys Leu Lys His Leu Xaa Leu Thr Ser Cys Val Ser Ile Thr Asn Ser
      145            150            155            160

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Ser Leu Lys Gly Ile Ser Glu Gly Cys Arg Asn Leu Glu Tyr Leu Asn  
 165 170 175  
 Leu Ser Trp Cys Asp Gln Ile Thr Lys Asp Gly Ile Glu Ala Leu Val  
 180 185 190  
 Arg Gly Cys Arg Gly Leu Lys Ala Leu Leu Leu Arg Gly Cys Thr Gln  
 195 200 205  
 Leu Glu Asp Glu Ala Leu Lys His Ile Gln Asn Tyr Cys His Glu Leu  
 210 215 220  
 Val Ser Leu Asn Leu Gln Ser Cys Ser Arg Ile Thr Asp Glu Gly Val  
 225 230 235 240  
 Val Gln Ile Cys Arg Gly Cys His Arg Leu Gln Ala Leu Cys Leu Ser  
 245 250 255  
 Gly Cys Ser Asn Leu Thr Asp Ala Ser Leu Thr Ala Leu Gly Leu Asn  
 260 265 270  
 Cys Pro Arg Leu Gln Ile Leu Glu Ala Ala Arg Cys Ser His Leu Thr  
 275 280 285  
 Asp Ala Gly Phe Thr Leu Leu Ala Arg Asn Cys His Glu Leu Glu Lys  
 290 295 300  
 Met Asp Leu Glu Xaa Cys Ile Leu Ile Thr Asp Ser Thr Leu Ile Gln  
 305 310 315 320  
 Leu Ser Ile His Cys Pro Lys Leu Gln Ala Leu Ser Leu Ser His Cys  
 325 330 335  
 Glu Leu Ile Xaa Asp Asp Gly Ile Leu His Leu Ser Asn Ser Thr Cys  
 340 345 350  
 Gly His Glu Arg Leu Arg Val Leu Glu Leu Asp Asn Cys Leu Leu Ile  
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 Thr Asp Val Ala Leu Xaa His Leu Glu Asn Cys Arg Gly Leu Glu Arg  
 370 375 380  
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 385 390 395 400  
 Met Arg Ala Gln Leu Pro His Val Lys Val His Ala Tyr Phe Ala Pro  
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 Cys Cys Val Ile Leu  
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<210> 55

<211> 1866

<212> DNA

<213> Homo sapiens

<400> 55

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 aacagccaga cttccctct caatgcagag gtatgccagt atgccaaaga agtagtggt 180  
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 gggacatggg gggatcagtg tcctagtgtc tccttgccat tcaagaggac gccacctaata 360  
 tttcagagcc aggactatgt ggaacttact tttgaacaac aggtgtatcc tacagctgta 420  
 catgttctag aaacctatca tcccggagca gtcattagaa ttctcgcttg ttctgcaaat 480  
 ccttattccc caaatccacc agctgaagta agatgggaga ttctttggtc agagagacct 540  
 acgaagggtga atgcttccca agctcgccag tttaaacctt gtattaagca gataaatttc 600  
 cccacaaatc ttatacgact ggaagttaat agttctcttc tggaatatta cactgaatta 660  
 gatgcagttg tgctacatgg tgtgaaggac aagccagtgc tttctctcaa gacttcactt 720  
 attgacatga atgatataga agatgatgcc tatgcagaaa aggatgggtg tggaatggac 780  
 agtcttaaca aaaagtttag cagtgtgtgc ctccggggaag ggccaaataa tgggtatttt 840  
 gataaactac cttatgagct tattcagctg attctgaatc atcttacct accagacctg 900  
 tgtagattag cacagacttg caaactactg agccagcatt gctgtgatcc tctgcaatac 960  
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<210> 56

<211> 621

<212> PRT

<213> Homo sapiens

<400> 56

Met Ser Pro Val Phe Pro Met Leu Thr Val Leu Thr Met Phe Tyr Tyr  
1 5 10 15

Ile Cys Leu Arg Arg Arg Ala Arg Thr Ala Thr Arg Gly Glu Met Met  
20 25 30

Asn Thr His Arg Ala Ile Glu Ser Asn Ser Gln Thr Ser Pro Leu Asn  
35 40 45

Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His  
50 55 60

Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly  
65 70 75 80

Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val  
85 90 95

Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu  
100 105 110

Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu





Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly Ser Cys Val Met Ile  
450 455 460  
Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys  
465 470 475 480  
Leu Arg Thr Leu Asp Leu Trp Arg Cys Lys Asn Ile Thr Glu Asn Gly  
485 490 495  
Ile Ala Glu Leu Ala Ser Gly Cys Pro Leu Leu Glu Glu Leu Asp Leu  
500 505 510  
Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu  
515 520 525  
Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg  
530 535 540  
Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg  
545 550 555 560  
Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser  
565 570 575  
Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val  
580 585 590  
Ser Phe Cys Ser Gln Ile Asp Asn Arg Ala Val Leu Glu Leu Asn Ala  
595 600 605  
Ser Phe Pro Lys Val Phe Ile Lys Lys Ser Phe Thr Gln  
610 615 620

<210> 57  
<211> 984  
<212> DNA  
<213> Homo sapiens

<400> 57  
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tctacttccc agcagcaact cacatttcag gagtctgtgc ttaaactgtg tcagcctgag 180  
cttgagagca gtcagattca catatcagtg ctgccaatgg aggtcctgat gtacatcttc 240  
cgatgggtgg tgtctagtga cttggacctc agatcattgg agcagttgtc gctgggtgtgc 300  
agaggattct acatctgtgc cagagaccct gaaatatggc gtctggcctg cttgaaagtt 360  
tggggcagaa gctgtattaa acttgttccg tacacgtcct ggagagagat gtttttagaa 420  
cggcctcgtg ttcggtttga tggcgtgtat atcagtaaaa ccacatatat tcgtcaaggg 480  
gaacagtctc ttgatggttt ctatagagcc tggcaccaag tggaatatta caggtacata 540  
agattctttc ctgatggcca tgtgatgatg ttgacaaccc ctgaagagcc tcagtccatt 600  
gttccacggt taagaactag gaataccagg actgatgcaa ttctactggg tcaactatgc 660  
ttgtcacaag acacagacaa tcagaccaa gtatttgctg taataactaa gaaaaaagaa 720  
gaaaaaccac ttgactataa atacagatat tttcgtcgtg tccctgtaca agaagcagat 780  
cagagttttc atgtggggct acagctatgt tccagtgggc accagagggt caacaaactc 840  
atctggatac atcattcttg tcacattact taaaaatcaa ctggtgagac tgcagtcagt 900  
gcttttgaga ttgacaagat gtacaccccc ttgttcttcg ccagagtaag gagctacaca 960  
gctttctcag aaaggcctct gtag 984

<210> 58  
<211> 327

<212> PRT

<213> Homo sapiens

<400> 58

Met Gln Leu Val Pro Asp Ile Glu Phe Lys Ile Thr Tyr Thr Arg Ser  
1 5 10 15

Pro Asp Gly Asp Gly Val Gly Asn Ser Tyr Ile Glu Asp Asn Asp Asp  
20 25 30

Asp Ser Lys Met Ala Asp Leu Leu Ser Tyr Phe Gln Gln Gln Leu Thr  
35 40 45

Phe Gln Glu Ser Val Leu Lys Leu Cys Gln Pro Glu Leu Glu Ser Ser  
50 55 60

Gln Ile His Ile Ser Val Leu Pro Met Glu Val Leu Met Tyr Ile Phe  
65 70 75 80

85 90 95

Ser Leu Val Cys Arg Gly Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile  
100 105 110

Trp Arg Leu Ala Cys Leu Lys Val Trp Gly Arg Ser Cys Ile Lys Leu  
115 120 125

Val Pro Tyr Thr Ser Trp Arg Glu Met Phe Leu Glu Arg Pro Arg Val  
130 135 140

Arg Phe Asp Gly Val Tyr Ile Ser Lys Thr Thr Tyr Ile Arg Gln Gly  
145 150 155 160

Glu Gln Ser Leu Asp Gly Phe Tyr Arg Ala Trp His Gln Val Glu Tyr  
165 170 175

Tyr Arg Tyr Ile Arg Phe Phe Pro Asp Gly His Val Met Met Leu Thr  
180 185 190

Thr Pro Glu Glu Pro Gln Ser Ile Val Pro Arg Leu Arg Thr Arg Asn  
195 200 205

Thr Arg Thr Asp Ala Ile Leu Leu Gly His Tyr Arg Leu Ser Gln Asp  
210 215 220

Thr Asp Asn Gln Thr Lys Val Phe Ala Val Ile Thr Lys Lys Lys Glu  
225 230 235 240

Glu Lys Pro Leu Asp Tyr Lys Tyr Arg Tyr Phe Arg Arg Val Pro Val  
245 250 255

Gln Glu Ala Asp Gln Ser Phe His Val Gly Leu Gln Leu Cys Ser Ser  
260 265 270

Gly His Gln Arg Phe Asn Lys Leu Ile Trp Ile His His Ser Cys His  
275 280 285

Ile Thr Tyr Lys Ser Thr Gly Glu Thr Ala Val Ser Ala Phe Glu Ile  
290 295 300

Asp Lys Met Tyr Thr Pro Leu Phe Phe Ala Arg Val Arg Ser Tyr Thr

305

310

315

320

Ala Phe Ser Glu Arg Pro Leu  
325

&lt;210&gt; 59

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; all n positions

&lt;223&gt; n=a, c, g or t

&lt;400&gt; 59

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gcagccctgg atcctgactt agagaatgat gatttctttg tcagaaagac tggggctttc 60
catgcaaadc catatgttct ccgagctttt gaagacttta gaaagtcttc tgagcaagat 120
gattctgtag agcgagatat aattttacag tgtagagaag gtgaacttgt acttccggat 180
ttggaaaaag atgatatgat tgttcgccga atcccagcac agaagaaaga agtgccgctg 240
tctggggccc cagatagata ccacccagtc ccttttcccg aaccctggac tcttccctcca 300
gaaattcaag caaaatttct ctgtgtactt gaaaggacat gcccatccaa agaaaaaagt 360
aatagctgta gaattattagt tccttcatat cggcagaaga aagatgacat gctgacacgt 420
aagattcagt cctggaaact gggaactacc gtgcctccca tcagtctcac ncctggcccc 480
tgcatgagg ctgacttgaa gagatgggag gccatccggg aggccagcag actcaggcac 540
aagaaaaggc tgatggtgga gagactcttt caaaagattt atggtgagaa tgggagtaag 600
tccatgagtg atgtcagcgc agaagatggt caaaacttgc gtcagctgcg ttacaggagg 660
atgcagaaaa taaaatcaca attaaaagaa caagatcaga aatggcagga tgaccttgca 720
aaatggaaaag atcgtcgaaa aagttacact tcagatctgc agaag 765
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&lt;210&gt; 60

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 60

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Ala Ala Leu Asp Pro Asp Leu Glu Asn Asp Asp Phe Phe Val Arg Lys
  1              5              10              15

Thr Gly Ala Phe His Ala Asn Pro Tyr Val Leu Arg Ala Phe Glu Asp
      20              25              30

Phe Arg Lys Phe Ser Glu Gln Asp Asp Ser Val Glu Arg Asp Ile Ile
      35              40              45

Leu Gln Cys Arg Glu Gly Glu Leu Val Leu Pro Asp Leu Glu Lys Asp
      50              55              60

Asp Met Ile Val Arg Arg Ile Pro Ala Gln Lys Lys Glu Val Pro Leu
      65              70              75              80

Ser Gly Ala Pro Asp Arg Tyr His Pro Val Pro Phe Pro Glu Pro Trp
      85              90              95

Thr Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg
      100             105             110

Thr Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro
      115             120             125
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Ser Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser  
 130 135 140  
 Trp Lys Leu Gly Thr Thr Val Pro Pro Ile Ser Phe Thr Pro Gly Pro  
 145 150 155 160  
 Cys Ser Glu Ala Asp Leu Lys Arg Trp Glu Ala Ile Arg Glu Ala Ser  
 165 170 175  
 Arg Leu Arg His Lys Lys Arg Leu Met Val Glu Arg Leu Phe Gln Lys  
 180 185 190  
 Ile Tyr Gly Glu Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu  
 195 200 205  
 Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile  
 210 215 220  
 Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala  
 225 230 235 240  
 Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys  
 245 250 255

<210> 61  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<400> 61  
 Leu Pro Pro Glu Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr  
 1 5 10 15  
 Asp Leu Cys Leu Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu  
 20 25 30  
 Leu Leu Trp Gln  
 35

<210> 62  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr  
 1 5 10 15  
 Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu  
 20 25 30  
 Leu Cys Gln Ser Ser Gly Lys Val Trp Lys  
 35 40

<210> 63  
 <211> 44  
 <212> PRT  
 <213> Homo sapiens

<400> 63

Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala Lys Ala  
1 5 10 15

Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys Val Arg  
20 25 30

Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile  
35 40

<210> 64

<211> 39

<212> PRT

<213> Homo sapiens

<400> 64

Leu Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln  
1 5 10 15

Asp Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala  
20 25 30

Asn Asp Pro Asn Leu Trp Lys  
35

<210> 65

<211> 41

<212> PRT

<213> Homo sapiens

<400> 65

Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala Tyr Leu His Leu Pro  
1 5 10 15

Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala Trp Tyr Glu Leu Ile  
20 25 30

Leu Ser Leu Asp Ser Thr Arg Trp Arg  
35 40

<210> 66

<211> 39

<212> PRT

<213> Homo sapiens

<400> 66

Leu Pro Thr Asp Pro Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg  
1 5 10 15

Asp Leu Ile Asn Cys Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser  
20 25 30

Ser His Asp Pro Leu Trp Arg  
35

<210> 67

<211> 40  
<212> PRT  
<213> Homo sapiens

<400> 67  
Leu Pro Glu Pro Leu Leu Leu Arg Val Leu Ala Ala Leu Pro Ala Ala  
1 5 10 15  
Glu Leu Val Gln Ala Cys Arg Leu Val Cys Leu Arg Trp Lys Glu Leu  
20 25 30  
Val Asp Gly Ala Pro Leu Trp Leu  
35 40

<210> 68  
<211> 40  
<212> PRT  
<213> Homo sapiens

<400> 68  
Leu Phe Pro Pro Glu Leu Val Glu His Ile Ile Ser Phe Leu Pro Val  
1 5 10 15  
Arg Asp Leu Val Ala Leu Gly Gln Thr Cys Arg Tyr Phe His Glu Val  
20 25 30  
Cys Asp Gly Glu Gly Val Trp Arg  
35 40

<210> 69  
<211> 44  
<212> PRT  
<213> Homo sapiens

<400> 69  
Leu Pro Glu Val Leu Leu Leu His Met Cys Ser Tyr Leu Asp Met Arg  
1 5 10 15  
Ala Leu Gly Arg Leu Ala Gln Val Tyr Arg Trp Leu Trp His Phe Thr  
20 25 30  
Asn Cys Asp Leu Leu Arg Arg Gln Ile Ala Trp Ala  
35 40

<210> 70  
<211> 40  
<212> PRT  
<213> Homo sapiens

<400> 70  
Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly  
1 5 10 15  
Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu  
20 25 30  
Ser Glu Asp Arg Gln Leu Trp Lys  
35 40

<210> 71  
<211> 39  
<212> PRT  
<213> Homo sapiens

<400> 71  
Leu Pro Asp His Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn  
1 5 10 15  
Gln Leu Cys Arg Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala  
20 25 30  
Trp Asp Pro Arg Leu Trp Arg  
35

<210> 72  
<211> 44  
<212> PRT  
<213> Homo sapiens

<400> 72  
Ile Pro Leu Glu Ile Leu Val Gln Ile Phe Gly Leu Leu Val Ala Ala  
1 5 10 15  
Asp Gly Pro Met Pro Phe Leu Gly Arg Ala Ala Arg Val Cys Arg Arg  
20 25 30  
Trp Gln Glu Ala Ala Ser Gln Pro Ala Leu Trp His  
35 40

<210> 73  
<211> 39  
<212> PRT  
<213> Homo sapiens

<400> 73  
Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu Asn Pro Gln  
1 5 10 15  
Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser Gln Leu Thr  
20 25 30  
Lys Thr Gly Ser Leu Trp Lys  
35

<210> 74  
<211> 39  
<212> PRT  
<213> Homo sapiens

<400> 74  
Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val  
1 5 10 15  
Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala  
20 25 30

Leu Asp Gly Ser Asn Trp Gln  
35

<210> 75

<211> 48

<212> PRT

<213> Homo sapiens

<400> 75

Leu Pro Tyr Glu Leu Ile Gln Leu Ile Leu Asn His Leu Thr Leu Pro  
1 5 10 15

Asp Leu Cys Arg Leu Ala Gln Thr Cys Lys Leu Leu Ser Gln His Cys  
20 25 30

Cys Asp Pro Leu Gln Tyr Ile His Leu Asn Leu Gln Pro Tyr Trp Ala  
35 40 45

<210> 76

<211> 44

<212> PRT

<213> Homo sapiens

<400> 76

Leu Pro Met Glu Val Leu Met Tyr Ile Phe Arg Trp Val Val Ser Ser  
1 5 10 15

Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu Ser Leu Val Cys Arg Gly  
20 25 30

Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile Trp Arg  
35 40

<210> 77

<211> 49

<212> PRT

<213> Homo sapiens

<400> 77

Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg Thr  
1 5 10 15

Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro Ser  
20 25 30

Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser Trp  
35 40 45

Lys

<210> 78

<211> 39

<212> PRT



<213> Homo sapiens

<400> 78

Leu Pro His His Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu  
1 5 10 15

Asp Arg Ala Cys Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe  
20 25 30

His Ile Ser Asp Leu Trp Arg  
35

<210> 79

<211> 43

<212> PRT

<213> Homo sapiens

<400> 79

Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile Ser Ala Leu  
1 5 10 15

Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys Gly Ser Trp  
20 25 30

Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala  
35 40

<210> 80

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 80

agtagtaaca aaggtaaaag acagttgact gtatcgtcga ggatgccttc aattaagtt 59

<210> 81

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 81

gcgggttactt acttagagct cgacgtctta cttacttagc tcacttctct tcacacca 58

<210> 82

<211> 12

<212> PRT

<213> Homo sapiens

<400> 82

Cys Asp Gly Glu Lys Asp Thr Tyr Ser Tyr Leu Ala  
1 5 10

<210> 83  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 83  
Cys Glu Ser Ser Phe Ser Leu Asn Met Asn Phe Ser Ser Lys Arg Thr  
1 5 10 15

Lys Phe Lys Ile Thr Thr Ser Met Gln  
20 25

<210> 84  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 84  
Cys Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp  
1 5 10

<210> 85  
<211> 19  
<212> PRT  
<213> Homo sapiens

<220>  
<221> Phosphorylation  
<222> 8  
<223> Phosothreonine

<400> 85  
Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly Leu Arg Arg  
1 5 10 15

Arg Gln Thr

<210> 86  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 86  
cctgggggat gttctca

17

<210> 87  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 87

ggcttccggg catttag

17

<210> 88

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 88

catctggcac gattcca

17

<210> 89

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 89

ccgctcatcg tatgaca

17

<210> 90

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> Phosphorylation

<222> 8

<223> Phosotyrosine

<400> 90

Ala Glu Ile Gly Val Gly Ala Tyr Gly Thr Val Tyr Lys Ala Arg Asp  
1 5 10 15

Pro His Ser